

DB 61 IQPFGRLALGKGLANDCLHBEYVGRDKCYTEDIIVLQDTRKTYSGRHFRIQ 120
 QY 121 ELGHSRVRANIEDSGNGTFVNEKIIIGKRTLELTNNALIALSTNNVPPSLSVD 180
 DB 121 ELGHSRVRANIEDSGNGTFVNEKIIIGKRTLELTNNALIALSTNNVPPSLSVD 180
 QY 181 QTIYPDPIDKYMSPRIGSACGEVKLAFOKSVCKKVAVKIISKRFKNTSSNEHPIS 240
 DB 181 QTIYPDPIDKYMSPRIGSACGEVKLAFOKSVCKKVAVKIISKRFKNTSSNEHPIS 240
 QY 241 VDTREILKGLDHPICIKIENPPOSEDPYIVLELMGGELPDRVNSTRLRPIALYF 300
 DB 241 VDTREILKGLDHPICIKIENPPOSEDPYIVLELMGGELPDRVNSTRLRPIALYF 300
 QY 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSECCIKITDPCGSKILGETSLMRTLCGTP 360
 DB 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSECCIKITDPCGSKILGETSLMRTLCGTP 360
 QY 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPSEBONSNIPLKQIAREKTYI 420
 DB 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPSEBONSNIPLKQIAREKTYI 420
 QY 421 AAAMRVSRQAPDLVKNLLVDPBQRLLTKQALEHPILODSSMGTVERLMTGVDTMTP 480
 DB 421 AAAMRVSRQAPDLVKNLLVDPBQRLLTKQALEHPILODSSMGTVERLMTGVDTMTP 480
 QY 481 PIKONIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517
 DB 481 PIKONIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517

RESULT 2
 Q98TW0 PRELIMINARY PRT; 517 AA.
 AC Q98TW0 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 GN Protein kinase Cdel.
 GN Name=Cdel;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodidae; Xenopus.
 NC NCBI_TaxID=8335;
 RN RN
 RA Matsumi T., Nakano H., Takisawa H.,
 RA Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DB EMBL; AF26574; AAC59884.1; -
 DB HSP; 096017; IGC.
 DR CO: GO:0005524; P-ATP binding; IEA.
 DR CO: GO:0004674; P-protein serine/threonine kinase activity; IEA.
 DR CO: GO:0016740; P:transferase activity; IEA.
 DR GO: GO:0006688; P:protein amino acid phosphorylation; IEA.
 DR InterPro: IPR002353; FHA.
 DR InterPro: IPR011009; Kinase like.
 DR InterPro: IPR00719; Prot kinase.
 DR InterPro: IPR002290; Ser-Thr kinase.
 DR InterPro: IPR008271; Ser-Thr_pkin_AS.
 DR InterPro: IPR008984; SMD_FHA.
 DR Pfam: PF00498; FHA; 1.
 DR Pfam: PF00069; Kinase; 1.
 DR ProDom: PD000001; Prot_kinase; 1.
 DR SMART: SM00240; FHA; 1.
 DR SMART: SM00240; S_TKc; 1.
 DR PROSITE: PS00006; FHA_DOMAIN; 1.
 DR PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
 KM ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
 SQ SOURCE 517 AA; 58310 MW; 401A335AA0BC8B C64;

Query Match 99.7%; Score 2704; DB 2; Length 517;
 Best Local Similarity 99.8%; Pred. No. 4,56-164;
 Matches 516; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MMSRDTKTESQSSQCTSSSSSSSAPQSTSSSSSCTLSLDTVPVQDLASIPDPRIED 60
 DB 1 MMSRDTKTESQSSQCTSSSSSSSAPQSTSSSSSCTLSLDTVPVQDLASIPDPRIED 60
 QY 61 IQPFGRLALGKGLANDCLHBEYVGRDKCYTEDIIVLQDTRKTYSGRHFRIQ 120
 DB 61 IQPFGRLALGKGLANDCLHBEYVGRDKCYTEDIIVLQDTRKTYSGRHFRIQ 120
 QY 121 ELGHSRVRANIEDSGNGTFVNEKIIIGKRTLELTNNALIALSTNNVPPSLSVD 180
 DB 121 ELGHSRVRANIEDSGNGTFVNEKIIIGKRTLELTNNALIALSTNNVPPSLSVD 180
 QY 181 QTIYPDPIDKYMSPRIGSACGEVKLAFOKSVCKKVAVKIISKRFKNTSSNEHPIS 240
 DB 181 QTIYPDPIDKYMSPRIGSACGEVKLAFOKSVCKKVAVKIISKRFKNTSSNEHPIS 240
 QY 241 VDTREILKGLDHPICIKIENPPOSEDPYIVLELMGGELPDRVNSTRLRPIALYF 300
 DB 241 VDTREILKGLDHPICIKIENPPOSEDPYIVLELMGGELPDRVNSTRLRPIALYF 300
 QY 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSECCIKITDPCGSKILGETSLMRTLCGTP 360
 DB 301 YQMLAVOYLHNGVYIHRDLKPEVNLSTSECCIKITDPCGSKILGETSLMRTLCGTP 360
 QY 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPSEBONSNIPLKQIAREKTYI 420
 DB 361 TYLAPEVLTAGTGYSSAVDCMSLGVILPVCLCGYPPSEBONSNIPLKQIAREKTYI 420
 QY 421 AAAMRVSRQAPDLVKNLLVDPBQRLLTKQALEHPILODSSMGTVERLMTGVDTMTP 480
 DB 421 AAAMRVSRQAPDLVKNLLVDPBQRLLTKQALEHPILODSSMGTVERLMTGVDTMTP 480
 QY 481 PIKONIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517
 DB 481 PIKONIIRKRGHEMDODASTSSCSSEILPITSABKRAK 517

RESULT 3
 CHK2_HUMAN STANDARD; PRT; 543 AA.
 AC Q96017; Q9UGF0; Q9UCP1;
 DT 30-MAY-2000 (Ref. 39, Created)
 DT 30-MAY-2000 (Ref. 39, Last sequence update)
 DT 25-OCT-2004 (Ref. 45, Last annotation update)
 DE Serine/threonine-protein kinase Chk2 (BC 2.7.1.37) (Cdel).
 GN Name=CHK2; Synonyms=CHK2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 NC NCBI_TaxID=9606;
 RN RN
 RA SEQUENCE FROM N.A.
 RA MEDLINE=99108191; PubMed=9889122; DOI=10.1016/S0960-9822(99)80041-4;
 RA Blaessle A., van de Weyer I., Laue W.C., Luyten W.R.M.L., Parker A.B.,
 RA McCowan C.H.;
 RA "A human homologue of the checkpoint kinase Cdel directly inhibits
 RT Cdc25 phosphatase.";
 RT Curr. Biol. 9:1-10(1999).
 RN RN
 RA SEQUENCE FROM N.A.
 RA MEDLINE=99055399; PubMed=9836640; DOI=10.1126/science.282.5395.1893;
 RA Matsuno S., Huang M., Ellledge S.J.;
 RT "Linkage of ATM to cell cycle regulation by the Chk2 protein kinase.";
 RL Science 282:1893-1897(1998).
 RN RN
 RA SEQUENCE FROM N.A.
 RA MEDLINE=99192255; PubMed=10097108; DOI=10.1073/pnas.96.7.3745;
 RA Brown A.L., Lee C.-H., Schwarz J.K., Mitiku N., Plimica-Worms H.,

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CC -----

DR EMBL, AJ131197, CA10319.1; -

DR EMBL, AF086904, AAC83693.1; -

DR EMBL, AF096379, AAD1784.1; -

DR EMBL, AF174135, AAD48504.1; -

DR EMBL, AL117330, CAB63923.1; -

DR EMBL, AL117325, CAB63922.1; -

DR EMBL, BC04207, AAH04207.1; -

DR PDB, 1GNC, X-ray; A/D/G/J=64-212.

DR Genew, HGNC:16627, CHEK2.

DR H-InvDB, HIX016341; -

DR Reactome, 096017; -

DR MIM, 604373; -

DR MIM, 151623; -

DR MIM, 176807; -

DR MIM, 259500; -

DR CO, GO:0005634, C:nucleus, NAS.

DR GO, GO:0004674, P:protein serine/threonine kinase activity, TAS.

DR GO, GO:0000077, P:DNA damage response, signal transduction re. .; TAS.

DR GO, GO:0006974, P:response to DNA damage stimulus, TAS.

DR InterPro, IPR000253, FHA.

DR InterPro, IPR011009, Prot_kinase.

DR InterPro, IPR000719, Kinase.

Query Match 61.0%; Score 1655.5; DB 1, Length 543;
Best Local Similarity 59.0%; Pred. No. 2.9e-97;
Matches 326; Conservative 74; Mismatches 105; Indels 39; Gaps 7;

QY 2 MSRDITKTESQ-----OSGTSSSSSSSAP-OSYSSSSSGTL 37
1 MSRSDEVAEQSHGSSACSPHGSVYSGSSSGSSGSISSSTSTPNSSQSHSSGTL 60

DB 38 SLSLDTVPVODLASI-----PEDPRTIDEDIPQPKRLALAKGPLANDCLHEIVFGKDK 92
61 SLELVSTOELYSIREDQEPEDQEEBETPAPKRLMALDQGFANLDCVANDNWFGRDSS 120

QY 93 CDYTDIPVLANOTDRKTYTSKRRPRIQELGHSRVANIEDLSGNGTVPNKEIYCKGRT 152
121 CERCEDEPLKRTDKRYTSKHFRIEFGVPKNSYAIYEDSGNGTFTVELVGKGR 180

QY 153 LPLTNNAETALSPLTNKVFPVSDLSVDQRTYPRDFIDKTYMRSPIGSGACGVKLAPOK 212
181 RPLNNSETALSLSNNKTFVFDLTVDQSVFPLALDSTYMKTLGSGACGVKLAPEK 240

QY 213 SVCKVAVVTKISKRPKMTSNEHP-1SDVTEILKLDHPCLIKINFPDSDFYI 271
241 KTCCKVALTKISKRPALGSAEADPALMVEETELIKLNPCLIKINFPDABD-VYI 299

QY 272 VLELMGEGELPDRVNSSTRLEAPIAKLYFYQMLAVOYLHNGVIRHDLKPEVLLSTS 331
300 VLELMGEGELPDKVGNRKLKATCKLYFYQMLAVOYLHNGIIRHDLKPEVLLSSE 359

QY 332 BECCIKITDPGSKILGISTLMRTLCGPTTYLABVLTAGTGYSAVDCMSLGYILFV 391
360 EECGLKITDPGSKILGISTLMRTLCGPTTYLABVLSVGTGYRAVDCMSLGYILF 419

QY 392 CLCGTPPSEBONSNIPLANOIABGKTYTYIAAMNVSSEDAFDLYKRLLVNDEBOLITQ 451
420 CLSGTPPSEBHTQVLSLQDQITSGKTFIPVMAFVEKALDVLKGLLVDPKARTTEE 479

QY 452 ALEHPLAODDSNIGHTVRLNYGVDTHTPP---1KKNIIKRGHEMDQDASISS-----C 503
480 ALRHNPLQDDEMKRFGQLSEENESTALPQVLAQFSTSHKRPBEGASGALSTYKPAVC 539

DB 504 SSIL 507

QY 540 AAVL 543

RESULT 4
098019

ID 098019 PRELIMINARY, PRT, 545 AA.
AC 098019
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Checkpoint kinase Chk2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
RX TTSURE-Thymus;
MDLINE=9361938; PubMed=10435585; DOI=10.1038/gsj.onc.1202925;
RA Chaturvedi P., Eng W.K., Zhu Y., Mactern M.R., Mishra R., Hurtle M.R., Zhang X., Annan R.S., Lu Q., Faucette L.F., Scott G.F., Li X., Carr S.A., Johnson R.K., Winkler J.D., Zhou B.B.;
RT "Mamalian Chk2 is a downstream effector of the ATM-dependent DNA damage checkpoint pathway".
RL Oncogene 18:4047-4054 (1999).
CC -1- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
DR EMBL: AF134054, BAD55890.1; -
DR HSP: 096017, 1GNC.
DR CO, GO:0005624, F:ATP binding, IEA.
DR CO, GO:0004674, P:protein serine/threonine kinase activity, IEA.
DR CO, GO:0016740, P:transferase activity, IEA.
DR CO, GO:0006968, P:protein amino acid phosphorylation, IEA.
DR InterPro, IPR000253, FHA.
DR InterPro, IPR011009, Kinase like.
DR InterPro, IPR000719, Prot_kinase.
DR InterPro, IPR002290, Ser_Thr_Pkinase.
DR InterPro, IPR008271, Ser_Thr_Pkin_AS.
DR InterPro, IPR008984, SMD_FHA.
DR Pfam, PF00438, FHA, 1.
DR Pfam, PF00693, PKinase, 1.
DR ProDom, PD000001, Prot_Kinase, 1.
DR SMART, SM00240, FHA, 1.
DR SMART, SM00220, S_TKC, 1.
DR PROSITE, PS50006, FHA DOMAIN, 1.
DR PROSITE, PS50011, PROTEIN KINASE DOM, 1.
DR PROSITE, PS00108, PROTEIN KINASE ST, 1.
KW ATP-binding; kinase; serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 545 AA; 60930 MW; CES32AD08068873 CRC64;

Query Match 60.6%; Score 1644.5; DB 2, Length 545;
Best Local Similarity 63.0%; Pred. No. 1.5e-96;
Matches 327; Conservative 69; Mismatches 108; Indels 15; Gaps 7;

QY 3 SRDTKTESQ-----OSGTSSSSSSSAP-OSYSSSSSGTSLDTVPVODLASIPEDPE 56
28 SSGSGTPSQDHLDSQYQASSSSTSTVPSGSSGSSSGTSLSELYSTOELQSIPEDE 87

DB 57 IDBDLPQPKRMLAKGKPLANDCLHEIVFGKDKDTPFDLPVLANOTDRKTYSGRR 116
88 PEEGPTPAPKRLMALQDPSNLDVNDYTFGRKSCBYCPDGLKRTKRYTSKRP 147

QY 117 RIFQSLGHSRVANIEDLSGNGTVPNKEIYCKGRTPLTNNAETALSPLTNKVFPVPSDL 176
148 RIFREKSPKNCYIYVLSDHSGNGTFTVELIGKRCPLSNNSETALSLSNNKTFVFDL 207

QY 177 SYVDQRTYPRDFIDKTYMRSPIGSGACGVKLAPOKSVCKKVAVKIISKRPMTSSN- 225
208 TDDQSVFPEKELDLYISKTLGSGACGVMAPEKTKCKVALIKISKRPALGSSREA 267

QY 236 EHPISVDTEILKLDHPCLIKINFPDSDFYIYLELMGEGELPDRVNSSTRLEPT 295
268 DTPASVETETELIKLKNPCLIKIKDVPDAB-VYIYLELMGEGELPDRVGNRKLSEAT 326

QY 296 AKLYFYQMLAVOYLHNGVIRHDLKPEVLLSSTSECCIKITDPGSKILGISTLMRT 355
327 CLKYFYQMLAVOYLHNGIIRHDLKPEVLLSSEBDCIKITDPGSKILGISTLMRT 386

QY 356 LCGPTTYLABVLTAGTGYSAVDCMSLGYILFVCLCGTPPSEBONSNIPLANOIABG 415